

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 28, 2006, 10:24:00 ; Search time 47 Seconds
(without alignments)
49.254 Million cell updates/sec

Title: US-10-809-144-10

Perfect score: 96
Sequence: 1 XXXXXXXXKFVRSRRPTASCALAFVN 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pdp.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pdp.*
- 3: /cgn2_6/prodata/1/iaa/7 COMB.pdp.*
- 4: /cgn2_6/prodata/1/iaa/8 COMB.pdp.*
- 5: /cgn2_6/prodata/1/iaa/9 COMB.pdp.*
- 6: /cgn2_6/prodata/1/iaa/10 COMB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	169	1	US-08-534-975-2
2	96	100.0	169	1	US-08-954-470-2
3	96	100.0	169	2	US-09-129-855A-2
4	96	100.0	169	2	US-09-247-154-2
5	96	100.0	169	2	US-09-480-718-2
6	96	100.0	169	2	US-09-610-833-2
7	96	100.0	169	2	US-09-129-855A-2
8	47	49.0	24	1	US-08-637-759B-495
9	47	49.0	24	2	US-08-871-355A-495
10	47	49.0	24	2	US-09-201-945-495
11	45	46.9	135	2	US-09-489-039A-279
12	45	46.9	303	2	US-09-252-991A-27884
13	44	45.8	146	2	US-09-252-991A-25680
14	43	44.8	326	2	US-09-252-991A-24487
15	42.5	44.3	108	2	US-08-189-039A-12459
16	42	43.8	314	2	US-09-252-991A-23723
17	42	43.8	1702	2	US-09-854-133-434
18	41	42.7	304	2	US-09-252-991A-31805
19	41	42.7	386	2	US-09-252-991A-27940
20	41	42.7	402	2	US-09-252-991A-30252
21	41	42.7	509	2	US-09-270-767-43544
22	41	42.7	841	2	US-09-270-767-45924
23	40	41.7	112	2	US-09-252-991A-26083
24	40	41.7	230	2	US-09-252-991A-28574
25	40	41.7	276	2	US-09-252-991A-20156
26	40	41.7	486	2	US-09-252-991A-31829
27	39	40.6	63	2	US-09-621-976-6007

28	39	40.6	119	2	US-09-270-767-43672	Sequence 43672, A
29	39	40.6	133	2	US-09-252-991A-26211	Sequence 26211, A
30	39	40.6	152	2	US-09-252-991A-17242	Sequence 17242, A
31	39	40.6	164	2	US-09-252-991A-16730	Sequence 16730, A
32	39	40.6	182	2	US-09-252-991A-23155	Sequence 23155, A
33	39	40.6	213	2	US-09-252-991A-19422	Sequence 19422, A
34	39	40.6	233	2	US-09-252-991A-23155	Sequence 23155, A
35	39	40.6	300	2	US-09-252-991A-19422	Sequence 19422, A
36	39	40.6	355	1	US-08-411-314C-2	Sequence 2, Appli
37	39	40.6	446	2	US-09-270-767-57633	Sequence 57633, A
38	39	40.6	466	2	US-09-270-767-42346	Sequence 42346, A
39	39	40.6	487	2	US-09-252-991A-29118	Sequence 29118, A
40	39	40.6	602	2	US-09-270-767-44887	Sequence 44887, A
41	38.5	40.1	638	2	US-09-252-991A-26597	Sequence 26597, A
42	38	39.6	108	2	US-09-328-352-5869	Sequence 5869, Ap
43	38	39.6	121	2	US-09-252-991A-28079	Sequence 28079, A
44	38	39.6	149	2	US-09-513-999C-4897	Sequence 4897, Ap
45	38	39.6	152	2	US-09-252-991A-25912	Sequence 25912, A

ALIGNMENTS

RESULT 1
US-08-534-975-2
; Sequence 2, Application US/08534975
; Patent No. 5723313
; GENERAL INFORMATION:

APPLICANT: Sherr, Charles, J.

APPLICANT: Quelle, Dawn, E.

TITLE OF INVENTION: ARF-p19, A No. 5723313el Regulator of the Mammalian Cell

TITLE OF INVENTION: Cycle

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/534,975

FILING DATE: 28-SEP-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Fox, Samuel, L.

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 0656.0590000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 169 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-534-975-2

Query Match 100.0%; Score 96; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KFYRSRRPTASCALAFVN 28

Db 26 KFYRSRRPTASCALAFVN 44